



SYR-HDAC-5005-C1 sub seq list 2.ST25
SEQUENCE LISTING

<110> Syrrx, Inc.

<120> HISTONE DEACETYLASE INHIBITORS

<130> SYR-HDAC-5005-C1

<140> US 10/803,575

<141> 2004-03-17

<150> US 60/455,437

<151> 2003-03-17

<150> US 60/531,203

<151> 2003-12-19

<160> 8

<170> PatentIn version 3.2

<210> 1

<211> 513

<212> PRT

<213> Artificial

<220>

<223> Residues 1-482 of HDAC1 with a "MSYYHHHHHDYDIPTTENLYFQGAMEPGGS"
tag at the N-terminus

<400> 1

Met Ser Tyr Tyr His His His His His His Asp Tyr Asp Ile Pro Thr
1 5 10 15

Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Glu Pro Gly Gly Ser Met
20 25 30

Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp Gly
35 40 45

Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His
50 55 60

Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr Arg
65 70 75 80

Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met Thr
85 90 95

Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg Pro
100 105 110

Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val Gly
115 120 125

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Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu Ser
 130 135 140
 Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln Thr
 145 150 155 160
 Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys Ser
 165 170 175
 Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile Leu
 180 185 190
 Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile
 195 200 205
 His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val
 210 215 220
 Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly
 225 230 235 240
 Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val Asn
 245 250 255
 Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
 260 265 270
 Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
 275 280 285
 Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
 290 295 300
 Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
 305 310 315 320
 Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr Ile
 325 330 335
 Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
 340 345 350
 Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
 355 360 365
 Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
 370 375 380

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Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
385 390 395 400

Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
405 410 415

Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro
420 425 430

Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
435 440 445

Glu Glu Phe Ser Asp Ser Glu Glu Gly Glu Gly Gly Arg Lys Asn
450 455 460

Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
465 470 475 480

Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
485 490 495

Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu
500 505 510

Ala

<210> 2
<211> 1542
<212> DNA
<213> Artificial

<220>
<223> DNA sequence encoding residues 1-482 of HDAC1 with a
"MSYYHHHHHDYDIPTTENLYFQGAMEPGGS" tag at the N-terminus

<400> 2
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tattttcagg gcgccatgga acccggggga tccatggcgc agacgcaggg caaccggagg 120
aaagtctgtt actactacga cggggatgtt ggaaattact attatggaca aggccacca 180
atgaagcctc accgaatccg catgactcat aatttgctgc tcaactatgg tctctaccga 240
aaaatggaaa tctatcgccc tcacaaagcc aatgctgagg agatgaccaa gtaccacagc 300
gatgactaca ttaaattctt gcgctccatc cgtccagata acatgtcgga gtacagcaag 360
cagatgcaga gattcaacgt tggtaggagc tgtccagtat tcgatggcct gtttgagttc 420
tgtcagttgt ctactggtgg ttctgtggca agtgctgtga aacttaataa gcagcagacg 480

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gacatcgctg tgaattgggc tgggggcctg caccatgcaa agaagtccga ggcattctggc 540
 ttctgttacg tcaatgatat cgtcttggcc atcctggaac tgctaaagta tcaccagagg 600
 gtgctgtaca ttgacattga tattcaccat ggtgacggcg tggaagaggc cttctacacc 660
 acggaccggg tcatgactgt gtcctttcat aagtatggag agtacttccc aggaactggg 720
 gacctacggg atatcggggc tggcaaaggc aagtattatg ctgttaacta cccgctccga 780
 gacgggattg atgacgagtc ctatgaggcc attttcaagc cggtcatgtc caaagtaatg 840
 gagatgttcc agcctagtgc ggtggtctta cagtgtggct cagactccct atctggggat 900
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 cttagaatgc tgccgcacgc acctggggtc caaatgcagg cgattcctga ggacgccatc 1260
 cctgaggaga gtggcgatga ggacgaagac gaccctgaca agcgcatctc gatctgctcc 1320
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 ggccgcaaga actcttccaa cttcaaaaaa gccaaagagag tcaaaacaga ggatgaaaaa 1440
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<210> 3
 <211> 498
 <212> PRT
 <213> Artificial

<220>
 <223> Residues 1-488 of HDAC2 with a "GHHHHH" tag at the C-terminus
 and a "MGS" tag at the N-terminus

<400> 3

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 1 5 10 15

Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His
 20 25 30

Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn
 35 40 45

Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr
 50 55 60

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Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu
65 70 75 80

Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln
85 90 95

Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu
100 105 110

Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
115 120 125

Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
130 135 140

His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
145 150 155 160

Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
165 170 175

Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr
180 185 190

Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr
195 200 205

Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys
210 215 220

Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser
225 230 235 240

Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr
245 250 255

Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly
260 265 270

Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys
275 280 285

Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly
290 295 300

Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
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atgaccata acttgctgtt aaattatggc ttatacagaa aaatggaaat atataggccc	180
cataaagcca ctgccgaaga aatgacaaaa tatcacagtg atgagtatat caaatttcta	240
cggtaataa gaccagataa catgtctgag tatagtaagc agatgcagag atttaatggt	300
ggagaagatt gtccagtgtt tgatggactc tttgagtttt gtcagctctc aactggcgg	360
tcagttgctg gagctgtgaa gttaaaccga caacagactg atatggctgt taattgggct	420
ggaggattac atcatgctaa gaaatcagaa gcatcaggat tctgttacgt taatgatatt	480
gtgcttgcca tccttgaatt actaaagtat catcagagag tcttatatat tgatatagat	540
attcatcatg gtgatggtgt tgaagaagct ttttatacaa cagatcgtgt aatgacggta	600
tcattccata aatatgggga atactttcct ggcacaggag acttgaggga tattggtgct	660
ggaaaaggca aatactatgc tgtcaatttt ccaatgagag atggtataga tgatgagtca	720
tatgggcaga ttttaagcc tattatctca aaggatgatg agatgtatca acctagtgt	780
gtggtattac agtgtggtgc agactcatta tctggtgata gactgggttg tttcaatcta	840
acagtcaaag gtcattgctaa atgtgtagaa gttgtaaaaa cttttaactt accattactg	900
atgcttgag gaggtggcta cacaatccgt aatgttgctc gatgttgagc atatgagact	960
gcagttgccc ttgattgtga gattcccaat gagttgccat ataattgatta ctttgagtat	1020
tttgaccag acttcaaact gcatattagt ccttcaaaca tgacaaacca gaacactcca	1080
gaatatatgg aaaagataaa acagcgtttg tttgaaaatt tgcgcatgtt acctcatgca	1140
cctggtgtcc agatgcaagc tattccagaa gatgctgttc atgaagacag tggagatgaa	1200
gatggagaag atccagacaa gagaatttct attcgagcat cagacaagcg gatagcttgt	1260
gatgaagaat tctcagattc tgaggatgaa ggagaaggag gtcgaagaaa tgtggctgat	1320
cataagaaag gagcaaagaa agctagaatt gaagaagata agaaagaaac agaggacaaa	1380
aaaacagacg ttaaggaaga agataaatcc aaggacaaca gtggtgaaaa aacagatacc	1440
aaaggaacca aatcagaaca gctcagcaac cccgggcac accatcacca tcactaa	1497

<210> 5

<211> 782

<212> PRT

<213> Artificial

<220>

<223> Residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-terminus and a "MP" tag at the N-terminus

<400> 5

Met	Pro	Gly	Met	Asp	Leu	Asn	Leu	Glu	Ala	Glu	Ala	Leu	Ala	Gly	Thr
1				5					10					15	

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Gly Leu Val Leu Asp Glu Gln Leu Asn Glu Phe His Cys Leu Trp Asp
20 25 30

Asp Ser Phe Pro Glu Gly Pro Glu Arg Leu His Ala Ile Lys Glu Gln
35 40 45

Leu Ile Gln Glu Gly Leu Leu Asp Arg Cys Val Ser Phe Gln Ala Arg
50 55 60

Phe Ala Glu Lys Glu Glu Leu Met Leu Val His Ser Leu Glu Tyr Ile
65 70 75 80

Asp Leu Met Glu Thr Thr Gln Tyr Met Asn Glu Gly Glu Leu Arg Val
85 90 95

Leu Ala Asp Thr Tyr Asp Ser Val Tyr Leu His Pro Asn Ser Tyr Ser
100 105 110

Cys Ala Cys Leu Ala Ser Gly Ser Val Leu Arg Leu Val Asp Ala Val
115 120 125

Leu Gly Ala Glu Ile Arg Asn Gly Met Ala Ile Ile Arg Pro Pro Gly
130 135 140

His His Ala Gln His Ser Leu Met Asp Gly Tyr Cys Met Phe Asn His
145 150 155 160

Val Ala Val Ala Ala Arg Tyr Ala Gln Gln Lys His Arg Ile Arg Arg
165 170 175

Val Leu Ile Val Asp Trp Asp Val His His Gly Gln Gly Thr Gln Phe
180 185 190

Thr Phe Asp Gln Asp Pro Ser Val Leu Tyr Phe Ser Ile His Arg Tyr
195 200 205

Glu Gln Gly Arg Phe Trp Pro His Leu Lys Ala Ser Asn Trp Ser Thr
210 215 220

Thr Gly Phe Gly Gln Gly Gln Gly Tyr Thr Ile Asn Val Pro Trp Asn
225 230 235 240

Gln Val Gly Met Arg Asp Ala Asp Tyr Ile Ala Ala Phe Leu His Val
245 250 255

Leu Leu Pro Val Ala Leu Glu Phe Gln Pro Gln Leu Val Leu Val Ala
260 265 270

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Ala Gly Phe Asp Ala Leu Gln Gly Asp Pro Lys Gly Glu Met Ala Ala
275 280 285

Thr Pro Ala Gly Phe Ala Gln Leu Thr His Leu Leu Met Gly Leu Ala
290 295 300

Gly Gly Lys Leu Ile Leu Ser Leu Glu Gly Gly Tyr Asn Leu Arg Ala
305 310 315 320

Leu Ala Glu Gly Val Ser Ala Ser Leu His Thr Leu Leu Gly Asp Pro
325 330 335

Cys Pro Met Leu Glu Ser Pro Gly Ala Pro Cys Arg Ser Ala Gln Ala
340 345 350

Ser Val Ser Cys Ala Leu Glu Ala Leu Glu Pro Phe Trp Glu Val Leu
355 360 365

Val Arg Ser Thr Glu Thr Val Glu Arg Asp Asn Met Glu Glu Asp Asn
370 375 380

Val Glu Glu Ser Glu Glu Glu Gly Pro Trp Glu Pro Pro Val Leu Pro
385 390 395 400

Ile Leu Thr Trp Pro Val Leu Gln Ser Arg Thr Gly Leu Val Tyr Asp
405 410 415

Gln Asn Met Met Asn His Cys Asn Leu Trp Asp Ser His His Pro Glu
420 425 430

Val Pro Gln Arg Ile Leu Arg Ile Met Cys Arg Leu Glu Glu Leu Gly
435 440 445

Leu Ala Gly Arg Cys Leu Thr Leu Thr Pro Arg Pro Ala Thr Glu Ala
450 455 460

Glu Leu Leu Thr Cys His Ser Ala Glu Tyr Val Gly His Leu Arg Ala
465 470 475 480

Thr Glu Lys Met Lys Thr Arg Glu Leu His Arg Glu Ser Ser Asn Phe
485 490 495

Asp Ser Ile Tyr Ile Cys Pro Ser Thr Phe Ala Cys Ala Gln Leu Ala
500 505 510

Thr Gly Ala Ala Cys Arg Leu Val Glu Ala Val Leu Ser Gly Glu Val
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515

520

525

Leu Asn Gly Ala Ala Val Val Arg Pro Pro Gly His His Ala Glu Gln
530 535 540

Asp Ala Ala Cys Gly Phe Cys Phe Phe Asn Ser Val Ala Val Ala Ala
545 550 555 560

Arg His Ala Gln Thr Ile Ser Gly His Ala Leu Arg Ile Leu Ile Val
565 570 575

Asp Trp Asp Val His His Gly Asn Gly Thr Gln His Met Phe Glu Asp
580 585 590

Asp Pro Ser Val Leu Tyr Val Ser Leu His Arg Tyr Asp His Gly Thr
595 600 605

Phe Phe Pro Met Gly Asp Glu Gly Ala Ser Ser Gln Ile Gly Arg Ala
610 615 620

Ala Gly Thr Gly Phe Thr Val Asn Val Ala Trp Asn Gly Pro Arg Met
625 630 635 640

Gly Asp Ala Asp Tyr Leu Ala Ala Trp His Arg Leu Val Leu Pro Ile
645 650 655

Ala Tyr Glu Phe Asn Pro Glu Leu Val Leu Val Ser Ala Gly Phe Asp
660 665 670

Ala Ala Arg Gly Asp Pro Leu Gly Gly Cys Gln Val Ser Pro Glu Gly
675 680 685

Tyr Ala His Leu Thr His Leu Leu Met Gly Leu Ala Ser Gly Arg Ile
690 695 700

Ile Leu Ile Leu Glu Gly Gly Tyr Asn Leu Thr Ser Ile Ser Glu Ser
705 710 715 720

Met Ala Ala Cys Thr Arg Ser Leu Leu Gly Asp Pro Pro Pro Leu Leu
725 730 735

Thr Leu Pro Arg Pro Pro Leu Ser Gly Ala Leu Ala Ser Ile Thr Glu
740 745 750

Thr Ile Gln Val His Arg Arg Tyr Trp Arg Ser Leu Arg Val Met Lys
755 760 765

SYR-HDAC-5005-C1 sub seq list 2.ST25
 Val Glu Asp Arg Glu Gly Pro Gly His His His His His His
 770 775 780

<210> 6
 <211> 2349
 <212> DNA
 <213> Artificial

<220>
 <223> DNA encoding residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-terminus and a "MP" tag at the N-terminus

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 cggctccatg ccatcaagga gcaactgatc caggagggcc tcctagatcg ctgcgtgtcc 180
 ttccaggccc ggtttgctga aaaggaagag ctgatgttg ttcacagcct agaatatatt 240
 gatctgatgg aaacaacca gtacatgaat gagggagaac tccgtgtcct agcagacacc 300
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 aggcctcctg gacatcacgc ccagcacagt cttatggatg gctattgcat gttcaaccac 480
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 gccacagagg ctgagctgct cacctgtcac agtgctgagt acgtgggtca tctccgggcc 1440
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atctgcccc gtaccttcgc ctgtgcacag cttgccactg gcgctgcctg ccgcctggtg 1560
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cacgcagagc aggatgcagc ttgcggtttt tgctttttca actctgtggc tgtggctgct 1680
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aaccagaac tgggtgctggt ctgagctggc tttgatgctg cacgggggga tccgctgggg 2040
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agtggccgca ttatccttat cctagagggg ggctataacc tgacatccat ctgagagtcc 2160
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ccccactat caggggccct ggcctcaatc actgagacca tccaagtcca tcgcagatac 2280
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catcactaa 2349

<210> 7

<211> 385

<212> PRT

<213> Artificial

<220>

<223> Residues 1-377 of HDAC8 with a "MHHHHHP" tag at the N-terminus

<400> 7

Met His His His His His His Pro Met Glu Glu Pro Glu Glu Pro Ala
1 5 10 15

Asp Ser Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr Ser Pro Glu Tyr
20 25 30

Val Ser Met Cys Asp Ser Leu Ala Lys Ile Pro Lys Arg Ala Ser Met
35 40 45

Val His Ser Leu Ile Glu Ala Tyr Ala Leu His Lys Gln Met Arg Ile
50 55 60

Val Lys Pro Lys Val Ala Ser Met Glu Glu Met Ala Ala Phe His Thr
65 70 75 80

Asp Ala Tyr Leu Gln His Leu Gln Lys Val Ser Gln Glu Gly Asp Asp

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85

90

95

Asp His Pro Asp Ser Ile Glu Tyr Gly Leu Gly Tyr Asp Cys Pro Ala
100 105 110

Thr Glu Gly Ile Phe Asp Tyr Ala Ala Ala Ile Gly Gly Ala Thr Ile
115 120 125

Thr Ala Ala Gln Cys Leu Ile Asp Gly Met Cys Lys Val Ala Ile Asn
130 135 140

Trp Ser Gly Gly Trp His His Ala Lys Lys Asp Glu Ala Ser Gly Phe
145 150 155 160

Cys Tyr Leu Asn Asp Ala Val Leu Gly Ile Leu Arg Leu Arg Arg Lys
165 170 175

Phe Glu Arg Ile Leu Tyr Val Asp Leu Asp Leu His His Gly Asp Gly
180 185 190

Val Glu Asp Ala Phe Ser Phe Thr Ser Lys Val Met Thr Val Ser Leu
195 200 205

His Lys Phe Ser Pro Gly Phe Phe Pro Gly Thr Gly Asp Val Ser Asp
210 215 220

Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn Val Pro Ile Gln
225 230 235 240

Asp Gly Ile Gln Asp Glu Lys Tyr Tyr Gln Ile Cys Glu Ser Val Leu
245 250 255

Lys Glu Val Tyr Gln Ala Phe Asn Pro Lys Ala Val Val Leu Gln Leu
260 265 270

Gly Ala Asp Thr Ile Ala Gly Asp Pro Met Cys Ser Phe Asn Met Thr
275 280 285

Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu Gln Trp Gln Leu
290 295 300

Ala Thr Leu Ile Leu Gly Gly Gly Gly Tyr Asn Leu Ala Asn Thr Ala
305 310 315 320

Arg Cys Trp Thr Tyr Leu Thr Gly Val Ile Leu Gly Lys Thr Leu Ser
325 330 335

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Ser Glu Ile Pro Asp His Glu Phe Phe Thr Ala Tyr Gly Pro Asp Tyr
340 345 350

Val Leu Glu Ile Thr Pro Ser Cys Arg Pro Asp Arg Asn Glu Pro His
355 360 365

Arg Ile Gln Gln Ile Leu Asn Tyr Ile Lys Gly Asn Leu Lys His Val
370 375 380

Val
385

<210> 8
<211> 1158
<212> DNA
<213> Artificial

<220>
<223> DNA encoding residues 1-377 of HDAC8 with a "MHHHHHP" tag at the N-terminus

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gatgcttata tgcagcatct ccagaaggct agccaagagg gcgatgatga tcatccggac 300
tccatagaat atgggctagg ttatgactgc ccagccactg aagggatatt tgactatgca 360
gcagctatag gaggggctac gatcacagct gcccaatgcc tgattgacgg aatgtgcaaa 420
gtagcaatta actggtcttg aggggtggcat catgcaaaga aagatgaagc atctgggtttt 480
tgttatctca atgatgctgt cctgggaata ttacgattgc gacggaaatt tgagcgtatt 540
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gacgtgtctg atgttggcct agggaaggga cgggtactaca gtgtaaatgt gcccattcag 720
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caagccttta atcccaaagc agtgggtctta cagctgggag ctgacacaat agctggggat 840
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cgatgctgga catacttgac cggggtcatc ctagggaata cactatcctc tgagatccca 1020
gatcatgagt ttttcacagc atatggctct gattatgtgc tggaaatcac gccaagctgc 1080
cggccagacc gcaatgagcc ccaccgaatc caacaaatcc tcaactacat caaagggaat 1140

SYR-HDAC-5005-C1 sub seq list 2.ST25

ctgaagcatg tggcttag

1158

SYR-HDAC-5005-C1 sub seq list 2.ST25
SEQUENCE LISTING

<110> Syrrx, Inc.

<120> HISTONE DEACETYLASE INHIBITORS

<130> SYR-HDAC-5005-C1

<140> US 10/803,575

<141> 2004-03-17

<150> US 60/455,437

<151> 2003-03-17

<150> US 60/531,203

<151> 2003-12-19

<160> 8

<170> PatentIn version 3.2

<210> 1

<211> 513

<212> PRT

<213> Artificial

<220>

<223> Residues 1-482 of HDAC1 with a "MSYYHHHHHDYDIPTTENLYFQGAMEPGGS"
tag at the N-terminus

<400> 1

Met Ser Tyr Tyr His His His His His His Asp Tyr Asp Ile Pro Thr
1 5 10 15

Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Glu Pro Gly Gly Ser Met
20 25 30

Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp Gly
35 40 45

Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His
50 55 60

Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr Arg
65 70 75 80

Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met Thr
85 90 95

Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg Pro
100 105 110

Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val Gly
115 120 125

SYR-HDAC-5005-C1 sub seq list 2.ST25

Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu Ser
 130 135 140
 Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln Thr
 145 150 155 160
 Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys Ser
 165 170 175
 Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile Leu
 180 185 190
 Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile
 195 200 205
 His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val
 210 215 220
 Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly
 225 230 235 240
 Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val Asn
 245 250 255
 Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
 260 265 270
 Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
 275 280 285
 Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
 290 295 300
 Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
 305 310 315 320
 Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr Ile
 325 330 335
 Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
 340 345 350
 Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
 355 360 365
 Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
 370 375 380

SYR-HDAC-5005-C1 sub seq list 2.ST25

Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
385 390 395 400

Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
405 410 415

Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro
420 425 430

Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
435 440 445

Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys Asn
450 455 460

Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
465 470 475 480

Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
485 490 495

Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu
500 505 510

Ala

<210> 2
<211> 1542
<212> DNA
<213> Artificial

<220>
<223> DNA sequence encoding residues 1-482 of HDAC1 with a
"MSYYHHHHHDYDIPTTENLYFQGAMEPGGS" tag at the N-terminus

<400> 2
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tattttcagg gcgccatgga acccggggga tccatggcgc agacgcaggg caccgggagg 120
aaagtctgtt actactacga cggggatgtt ggaaattact attatggaca aggccacca 180
atgaagcctc accgaatccg catgactcat aatttgctgc tcaactatgg tctctaccga 240
aaaatggaaa tctatcgccc tcacaaagcc aatgctgagg agatgaccaa gtaccacagc 300
gatgactaca ttaaattctt gcgctccatc cgtccagata acatgtcggg gtacagcaag 360
cagatgcaga gattcaacgt tggtagaggac tgtccagtat tcgatggcct gtttgagttc 420
tgtcagttgt ctactggtgg ttctgtggca agtgctgtga aacttaataa gcagcagacg 480

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gacatcgctg tgaattgggc tgggggcctg caccatgcaa agaagtccga ggcattctggc 540
 ttctgttacg tcaatgatat cgtcttggcc atcctggaac tgctaaagta tcaccagagg 600
 gtgctgtaca ttgacattga tattcaccat ggtgacggcg tggaagaggc cttctacacc 660
 acggaccggg tcatgactgt gtcctttcat aagtatggag agtacttccc aggaactggg 720
 gacctacggg atatcggggc tggcaaaggc aagtattatg ctgttaacta cccgctccga 780
 gacgggattg atgacgagtc ctatgaggcc attttcaagc cggtcattgtc caaagtaatg 840
 gagatgttcc agcctagtgc ggtggtctta cagtgtggct cagactccct atctggggat 900
 cggttagggtt gcttcaatct aactatcaaa ggacacgcca agtgtgtgga atttgtcaag 960
 agctttaacc tgcctatgct gatgctggga ggcgggtggtt acaccattcg taacgttgcc 1020
 cggtgctgga catatgagac agctgtggcc ctggatacgg agatccctaa tgagcttcca 1080
 tacaatgact actttgaata ctttggacca gatttcaagc tccacatcag tccttccaat 1140
 atgactaacc agaacacgaa tgagtacctg gagaagatca aacagcgact gtttgagaac 1200
 cttagaatgc tgccgcacgc acctgggggc caaatgcagg cgattcctga ggacgccatc 1260
 cctgaggaga gtggcgatga ggacgaagac gaccctgaca agcgcatctc gatctgctcc 1320
 tctgacaaac gaattgcctg tgaggaagag ttctccgatt ctgaagagga gggagagggg 1380
 ggccgcaaga actcttccaa cttcaaaaaa gccaagagag tcaaaacaga ggatgaaaaa 1440
 gagaaagacc cagaggagaa gaaagaagtc accgaagagg agaaaaccaa ggaggagaag 1500
 ccagaagcca aaggggtcaa ggaggagggtc aagttggcct ga 1542

<210> 3
 <211> 498
 <212> PRT
 <213> Artificial

<220>
 <223> Residues 1-488 of HDAC2 with a "GHHHHH" tag at the C-terminus
 and a "MGS" tag at the N-terminus

<400> 3

Met Gly Ser Met Ala Tyr Ser Gln Gly Gly Gly Lys Lys Lys Val Cys
 1 5 10 15

Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His
 20 25 30

Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn
 35 40 45

Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr
 50 55 60

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Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu
65 70 75 80

Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln
85 90 95

Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu
100 105 110

Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
115 120 125

Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
130 135 140

His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
145 150 155 160

Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
165 170 175

Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr
180 185 190

Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr
195 200 205

Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys
210 215 220

Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser
225 230 235 240

Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr
245 250 255

Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly
260 265 270

Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys
275 280 285

Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly
290 295 300

Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
Page 5

305 SYR-HDAC-5005-C1 sub seq list 2.ST25 310 315 320

Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
325 330 335

Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
340 345 350

Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
355 360 365

Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
370 375 380

Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
385 390 395 400

Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
405 410 415

Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
420 425 430

Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala
435 440 445

Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val
450 455 460

Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr
465 470 475 480

Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro Gly His His His His
485 490 495

His His

<210> 4
<211> 1497
<212> DNA
<213> Artificial

<220>
<223> DNA sequence encoding residues 1-488 of HDAC2 with a "GHHHHHH" tag at the C-terminus and a "MGS" tag at the N-terminus

<400> 4
atgggatcca tggcgtacag tcaaggaggc ggcaaaaaaa aagtctgcta ctactacgac 60

SYR-HDAC-5005-C1 sub seq list 2.ST25

ggtgatattg gaaattatta ttatggacag ggtcatccca tgaagcctca tagaatccgc	120
atgaccata acttgctgtt aaattatggc ttatacagaa aaatggaaat atatagggcc	180
cataaagcca ctgccgaaga aatgacaaaa tatcacagtg atgagtatat caaatttcta	240
cggtaataa gaccagataa catgtctgag tatagtaagc agatgcagag atttaatggt	300
ggagaagatt gtccagtgtt tgatggactc tttgagtttt gtcagctctc aactggcggg	360
tcagttgctg gagctgtgaa gttaaaccga caacagactg atatggctgt taattgggct	420
ggaggattac atcatgctaa gaaatcagaa gcatcaggat tctgttacgt taatgatatt	480
gtgcttgcca tccttgaatt actaaagtat catcagagag tcttatatat tgatatagat	540
attcatcatg gtgatgggtg tgaagaagct ttttatacaa cagatcgtgt aatgacggta	600
tcattccata aatatgggga atactttcct ggcacaggag acttgagggg tattgggtgct	660
ggaaaaggca aatactatgc tgtcaatttt ccaatgagag atggtataga tgatgagtca	720
tatgggcaga tatttaagcc tattatctca aagggtgatg agatgtatca acctagtgt	780
gtggtattac agtgtggtgc agactcatta tctggtgata gactgggttg tttcaatcta	840
acagtcaaag gtcattgctaa atgtgtagaa gttgtaaaaa cttttaactt accattactg	900
atgcttgagg gaggtggcta cacaatccgt aatgttgctc gatgttgga atatgagact	960
gcagttgccc ttgattgtga gattcccaat gagttgcat ataattgatta ctttgagtat	1020
tttgaccag acttcaaact gcatattagt ccttcaaaca tgacaaacca gaacactcca	1080
gaatatatgg aaaagataaa acagcgtttg tttgaaaatt tgcgcatgtt acctcatgca	1140
cctggtgtcc agatgcaagc tattccagaa gatgctgttc atgaagacag tggagatgaa	1200
gatggagaag atccagacaa gagaatttct attcgagcat cagacaagcg gatagcttgt	1260
gatgaagaat tctcagattc tgaggatgaa ggagaaggag gtcgaagaaa tgtggctgat	1320
cataagaaag gagcaaagaa agctagaatt gaagaagata agaaagaaac agaggacaaa	1380
aaaacagacg ttaaggaaga agataaatcc aaggacaaca gtggtgaaaa aacagatacc	1440
aaaggaacca aatcagaaca gctcagcaac cccgggcac accatcacca tcactaa	1497

<210> 5
 <211> 782
 <212> PRT
 <213> Artificial

<220>
 <223> Residues 73-845 of HDAC6 with a "GHHHHH" tag at the C-terminus
 and a "MP" tag at the N-terminus

<400> 5

Met	Pro	Gly	Met	Asp	Leu	Asn	Leu	Glu	Ala	Glu	Ala	Leu	Ala	Gly	Thr
1				5					10					15	

SYR-HDAC-5005-C1 sub seq list 2.ST25

Gly Leu Val₂₀ Leu Asp Glu Gln Leu₂₅ Asn Glu Phe His Cys₃₀ Leu Trp Asp
 Asp Ser Phe₃₅ Pro Glu Gly Pro₄₀ Glu Arg Leu His Ala Ile₄₅ Lys Glu Gln
 Leu Ile₅₀ Gln Glu Gly Leu₅₅ Leu Asp Arg Cys Val₆₀ Ser Phe Gln Ala Arg
 Phe Ala Glu Lys Glu₇₀ Glu Leu Met Leu Val₇₅ His Ser Leu Glu Tyr Ile₈₀
 Asp Leu Met Glu₈₅ Thr Thr Gln Tyr Met₉₀ Asn Glu Gly Glu Leu Arg Val₉₅
 Leu Ala Asp Thr₁₀₀ Tyr Asp Ser Val₁₀₅ Tyr Leu His Pro Asn Ser₁₁₀ Tyr Ser
 Cys Ala Cys₁₁₅ Leu Ala Ser Gly Ser₁₂₀ Val Leu Arg Leu Val₁₂₅ Asp Ala Val
 Leu Gly₁₃₀ Ala Glu Ile Arg Asn₁₃₅ Gly Met Ala Ile Ile₁₄₀ Arg Pro Pro Gly
 His His Ala Gln His Ser₁₅₀ Leu Met Asp Gly Tyr₁₅₅ Cys Met Phe Asn His₁₆₀
 Val Ala Val Ala₁₆₅ Arg Tyr Ala Gln Gln₁₇₀ Lys His Arg Ile Arg Arg₁₇₅
 Val Leu Ile Val₁₈₀ Asp Trp Asp Val₁₈₅ His His Gly Gln Gly Thr₁₉₀ Gln Phe
 Thr Phe Asp₁₉₅ Gln Asp Pro Ser Val₂₀₀ Leu Tyr Phe Ser Ile₂₀₅ His Arg Tyr
 Glu Gln Gly Arg Phe Trp Pro₂₁₅ His Leu Lys Ala Ser₂₂₀ Asn Trp Ser Thr
 Thr Gly Phe Gly Gln₂₃₀ Gly Gln Gly Tyr Thr Ile₂₃₅ Asn Val Pro Trp Asn₂₄₀
 Gln Val Gly Met Arg₂₄₅ Asp Ala Asp Tyr Ile₂₅₀ Ala Ala Phe Leu His Val₂₅₅
 Leu Leu Pro Val₂₆₀ Ala Leu Glu Phe Gln₂₆₅ Pro Gln Leu Val Leu₂₇₀ Val Ala

SYR-HDAC-5005-C1 sub seq list 2.ST25

Ala Gly Phe Asp Ala Leu Gln Gly Asp Pro Lys Gly Glu Met Ala Ala
275 280 285

Thr Pro Ala Gly Phe Ala Gln Leu Thr His Leu Leu Met Gly Leu Ala
290 295 300

Gly Gly Lys Leu Ile Leu Ser Leu Glu Gly Gly Tyr Asn Leu Arg Ala
305 310 315 320

Leu Ala Glu Gly Val Ser Ala Ser Leu His Thr Leu Leu Gly Asp Pro
325 330 335

Cys Pro Met Leu Glu Ser Pro Gly Ala Pro Cys Arg Ser Ala Gln Ala
340 345 350

Ser Val Ser Cys Ala Leu Glu Ala Leu Glu Pro Phe Trp Glu Val Leu
355 360 365

Val Arg Ser Thr Glu Thr Val Glu Arg Asp Asn Met Glu Glu Asp Asn
370 375 380

Val Glu Glu Ser Glu Glu Glu Gly Pro Trp Glu Pro Pro Val Leu Pro
385 390 395 400

Ile Leu Thr Trp Pro Val Leu Gln Ser Arg Thr Gly Leu Val Tyr Asp
405 410 415

Gln Asn Met Met Asn His Cys Asn Leu Trp Asp Ser His His Pro Glu
420 425 430

Val Pro Gln Arg Ile Leu Arg Ile Met Cys Arg Leu Glu Glu Leu Gly
435 440 445

Leu Ala Gly Arg Cys Leu Thr Leu Thr Pro Arg Pro Ala Thr Glu Ala
450 455 460

Glu Leu Leu Thr Cys His Ser Ala Glu Tyr Val Gly His Leu Arg Ala
465 470 475 480

Thr Glu Lys Met Lys Thr Arg Glu Leu His Arg Glu Ser Ser Asn Phe
485 490 495

Asp Ser Ile Tyr Ile Cys Pro Ser Thr Phe Ala Cys Ala Gln Leu Ala
500 505 510

Thr Gly Ala Ala Cys Arg Leu Val Glu Ala Val Leu Ser Gly Glu Val
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515

520

525

Leu Asn Gly Ala Ala Val Val Arg Pro Pro Gly His His Ala Glu Gln
530 535 540

Asp Ala Ala Cys Gly Phe Cys Phe Phe Asn Ser Val Ala Val Ala Ala
545 550 555 560

Arg His Ala Gln Thr Ile Ser Gly His Ala Leu Arg Ile Leu Ile Val
565 570 575

Asp Trp Asp Val His His Gly Asn Gly Thr Gln His Met Phe Glu Asp
580 585 590

Asp Pro Ser Val Leu Tyr Val Ser Leu His Arg Tyr Asp His Gly Thr
595 600 605

Phe Phe Pro Met Gly Asp Glu Gly Ala Ser Ser Gln Ile Gly Arg Ala
610 615 620

Ala Gly Thr Gly Phe Thr Val Asn Val Ala Trp Asn Gly Pro Arg Met
625 630 635 640

Gly Asp Ala Asp Tyr Leu Ala Ala Trp His Arg Leu Val Leu Pro Ile
645 650 655

Ala Tyr Glu Phe Asn Pro Glu Leu Val Leu Val Ser Ala Gly Phe Asp
660 665 670

Ala Ala Arg Gly Asp Pro Leu Gly Gly Cys Gln Val Ser Pro Glu Gly
675 680 685

Tyr Ala His Leu Thr His Leu Leu Met Gly Leu Ala Ser Gly Arg Ile
690 695 700

Ile Leu Ile Leu Glu Gly Gly Tyr Asn Leu Thr Ser Ile Ser Glu Ser
705 710 715 720

Met Ala Ala Cys Thr Arg Ser Leu Leu Gly Asp Pro Pro Pro Leu Leu
725 730 735

Thr Leu Pro Arg Pro Pro Leu Ser Gly Ala Leu Ala Ser Ile Thr Glu
740 745 750

Thr Ile Gln Val His Arg Arg Tyr Trp Arg Ser Leu Arg Val Met Lys
755 760 765

SYR-HDAC-5005-C1 sub seq list 2.ST25
 val Glu Asp Arg Glu Gly Pro Gly His His His His His His
 770 775 780

<210> 6
 <211> 2349
 <212> DNA
 <213> Artificial

<220>
 <223> DNA encoding residues 73-845 of HDAC6 with a "GHHHHH" tag at the C-terminus and a "MP" tag at the N-terminus

<400> 6
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 gatgagcagt taaatgaatt ccattgcctc tgggatgaca gcttcccgga aggccctgag 120
 cggctccatg ccatcaagga gcaactgata caggagggcc tcctagatcg ctgcgtgtcc 180
 ttccaggccc ggtttgctga aaaggaagag ctgatgttgg ttcacagcct agaatatatt 240
 gatctgatgg aaacaacca gtacatgaat gagggagaac tccgtgtcct agcagacacc 300
 tacgactcag tttatctgca tccgaactca tactcctgtg cctgcctggc ctcaggctct 360
 gtcctcaggc tgggtgatgc ggtcctgggg gctgagatcc ggaatggcat ggccatcatt 420
 aggcctcctg gacatcacgc ccagcacagt cttatggatg gctattgcat gttcaaccac 480
 gtggctgtgg cagcccgtca tgctcaacag aaacaccgca tccggagggt ccttatcgta 540
 gattgggatg tgcaccacgg tcaaggaaca cagttcacct tcgaccagga cccagtgctc 600
 ctctatttct ccatccaccg ctacgagcag ggtagggttct ggccccacct gaaggcctct 660
 aactggtcca ccacaggttt cggccaaggc caaggatata ccatcaatgt gccttggaac 720
 cagggtggga tgcgggatgc tgactacatt gctgctttcc tgcacgtcct gctgccagtc 780
 gccctcgagt tccagcctca gctggtcctg gtggctgtcg gatttgatgc cctgcaaggg 840
 gacccaagg gtgagatggc cgccactccg gcagggttcg cccagctaac ccacctgctc 900
 atgggtctgg caggaggcaa gctgatactg tctctggagg gtggctacaa cctccgcgcc 960
 ctggctgaag gcgtcagtgc ttcgtccac acccttcttg gagacccttg ccccatgctg 1020
 gagtcacctg gtgccccctg ccggagtgcc caggcttcag tttcctgtgc tctggaagcc 1080
 cttgagccct tctgggaggt tcttgtgaga tcaactgaga ccgtggagag ggacaacatg 1140
 gaggaggaca atgtagagga gagcgaggag gaaggaccct gggagcccc tgtgctccca 1200
 atcctgacat ggccagtgtc acagtctcgc acagggttg tctatgacca aaatatgatg 1260
 aatcactgca acttgtggga cagccaccac cctgaggtac cccagcgcac cttgcggatc 1320
 atgtgccgtc tggaggagct gggccttgcc gggcgctgcc tcaccctgac accgcgccct 1380
 gccacagagg ctgagctgct cacctgtcac agtgctgagt acgtgggtca tctccgggcc 1440
 acagagaaaa tgaaaaccg ggagctgcac cgtgagagtt ccaactttga ctccatctat 1500

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atctgccccca gtaccttcgc ctgtgcacag cttgccactg gcgctgcctg ccgcctggtg 1560
gaggctgtgc tctcaggaga ggttctgaat ggtgctgctg tgggtgcgtcc cccaggacac 1620
cacgcagagc aggatgcagc ttgcggtttt tgctttttca actctgtggc tgtggctgct 1680
cgccatgccc agactatcag tgggcatgcc ctacggatcc tgattgtgga ttgggatgtc 1740
caccacggta atggaactca gcacatgttt gaggatgacc ccagtgtgct atatgtgtcc 1800
ctgcaccgct atgatcatgg caccttcttc cccatggggg atgaggggtgc cagcagccag 1860
atcggccggg ctgcgggcac aggcttcacc gtcaacgtgg catggaacgg gccccgcatg 1920
ggtgatgctg actacctagc tgcctggcat cgcctggtgc ttcccattgc ctacgagttt 1980
aaccagaac tgggtgctggt ctacagctggc tttgatgctg cacgggggga tccgctgggg 2040
ggctgccagg tgtcacctga gggttatgcc cacctcacc acctgctgat gggccttgcc 2100
agtggccgca ttatccttat cctagagggg ggctataacc tgacatccat ctacagagtc 2160
atggctgcct gcactcgtc cctccttgga gaccaccac ccctgctgac cctgccacgg 2220
ccccactat caggggccct ggcctcaatc actgagacca tccaagtcca tcgcagatac 2280
tggcgcagct tacgggtcat gaaggtagaa gacagagaag gacccgggca tcaccatcac 2340
catcactaa 2349

<210> 7
<211> 385
<212> PRT
<213> Artificial

<220>
<223> Residues 1-377 of HDAC8 with a "MHHHHHP" tag at the N-terminus

<400> 7

Met His His His His His His Pro Met Glu Glu Pro Glu Glu Pro Ala
1 5 10 15

Asp Ser Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr Ser Pro Glu Tyr
20 25 30

Val Ser Met Cys Asp Ser Leu Ala Lys Ile Pro Lys Arg Ala Ser Met
35 40 45

Val His Ser Leu Ile Glu Ala Tyr Ala Leu His Lys Gln Met Arg Ile
50 55 60

Val Lys Pro Lys Val Ala Ser Met Glu Glu Met Ala Ala Phe His Thr
65 70 75 80

Asp Ala Tyr Leu Gln His Leu Gln Lys Val Ser Gln Glu Gly Asp Asp
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85

90

95

Asp His Pro Asp Ser Ile Glu Tyr Gly Leu Gly Tyr Asp Cys Pro Ala
100 105 110

Thr Glu Gly Ile Phe Asp Tyr Ala Ala Ala Ile Gly Gly Ala Thr Ile
115 120 125

Thr Ala Ala Gln Cys Leu Ile Asp Gly Met Cys Lys Val Ala Ile Asn
130 135 140

Trp Ser Gly Gly Trp His His Ala Lys Lys Asp Glu Ala Ser Gly Phe
145 150 155 160

Cys Tyr Leu Asn Asp Ala Val Leu Gly Ile Leu Arg Leu Arg Arg Lys
165 170 175

Phe Glu Arg Ile Leu Tyr Val Asp Leu Asp Leu His His Gly Asp Gly
180 185 190

Val Glu Asp Ala Phe Ser Phe Thr Ser Lys Val Met Thr Val Ser Leu
195 200 205

His Lys Phe Ser Pro Gly Phe Phe Pro Gly Thr Gly Asp Val Ser Asp
210 215 220

Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn Val Pro Ile Gln
225 230 235 240

Asp Gly Ile Gln Asp Glu Lys Tyr Tyr Gln Ile Cys Glu Ser Val Leu
245 250 255

Lys Glu Val Tyr Gln Ala Phe Asn Pro Lys Ala Val Val Leu Gln Leu
260 265 270

Gly Ala Asp Thr Ile Ala Gly Asp Pro Met Cys Ser Phe Asn Met Thr
275 280 285

Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu Gln Trp Gln Leu
290 295 300

Ala Thr Leu Ile Leu Gly Gly Gly Gly Tyr Asn Leu Ala Asn Thr Ala
305 310 315 320

Arg Cys Trp Thr Tyr Leu Thr Gly Val Ile Leu Gly Lys Thr Leu Ser
325 330 335

SYR-HDAC-5005-C1 sub seq list 2.ST25

Ser Glu Ile Pro Asp His Glu Phe Phe Thr Ala Tyr Gly Pro Asp Tyr
340 345 350

Val Leu Glu Ile Thr Pro Ser Cys Arg Pro Asp Arg Asn Glu Pro His
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Arg Ile Gln Gln Ile Leu Asn Tyr Ile Lys Gly Asn Leu Lys His Val
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Val
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SYR-HDAC-5005-C1 sub seq list 2.ST25

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